

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Stern, David M.
Yan, Shi Du
- (ii) TITLE OF INVENTION: AN INTRACELLULAR AMYLOID-BETA PEPTIDE
BINDING (ERAB) POLYPEPTIDE AND METHODS FOR INHIBITING
NEURODEGENERATIVE CONDITIONS
- (iii) NUMBER OF SEQUENCES: 5
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Cooper & Dunham LLP
(B) STREET: 1185 Avenue of the Americas
(C) CITY: New York
(D) STATE: NY
(E) COUNTRY: U.S.A.
(F) ZIP: 10036
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/815,225
(B) FILING DATE: 12-MAR-1997
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: White, John P.
(B) REGISTRATION NUMBER: 28,678
(C) REFERENCE/DOCKET NUMBER: 0575/55209
- (ix) TELECOMMUNICATION INFORMATION:
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(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 981 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
(A) NAME/KEY: CDS

(B) LOCATION: 19..801

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGAGTGGCCG GCGACAAG	ATG	GCA	GCA	GCG	TGT	CGG	AGC	GTG	AAG	GGC	CTG	51
	Met	Ala	Ala	Ala	Cys	Arg	Ser	Val	Lys	Gly	Leu	
	1				5					10		
GTG GCG GTA ATA ACC GGA GGA GCC TCG GGC CTG GGC CTG GCC ACG GCG												99
Val Ala Val Ile Thr Gly Gly Ala Ser Gly Leu Gly Leu Ala Thr Ala												
	15				20					25		
GAG CGA CTT GTG GGG CAG GGA GCC TCT GCT GTG CTT CTG GAC CTG CCC												147
Glu Arg Leu Val Gly Gln Gly Ala Ser Ala Val Leu Leu Asp Leu Pro												
	30				35					40		
AAC TCG GGT GGG GAG GCC CAA GCC AAG AAG TTA GGA AAC AAC TGC GTT												195
Asn Ser Gly Gly Glu Ala Gln Ala Lys Lys Leu Gly Asn Asn Cys Val												
	45				50					55		
TTC GCC CCA GCC GAC GTG ACC TCT GAG AAG GAT GTG CAA ACA GCT CTG												243
Phe Ala Pro Ala Asp Val Thr Ser Glu Lys Asp Val Gln Thr Ala Leu												
	60				65				70			75
GCT CTA GCA AAA GGA AAG TTT GGC CGT GTG GAT GTA GCT GTC AAC TGT												291
Ala Leu Ala Lys Gly Lys Phe Gly Arg Val Asp Val Ala Val Asn Cys												
	80							85			90	
GCA GGC ATC GCG GTG GCT AGC AAG ACG TAC AAC TTA AAG AAG GGC CAG												339
Ala Gly Ile Ala Val Ala Ser Lys Thr Tyr Asn Leu Lys Lys Gly Gln												
	95							100			105	
ACC CAT ACC TTG GAA GAC TTC CAG CGA GTT CTT GAT GTG AAT CTC ATG												387
Thr His Thr Leu Glu Asp Phe Gln Arg Val Leu Asp Val Asn Leu Met												
	110									120		
GGC ACC TTC AAT GTG ATC CGC CTG GTG GCT GGT GAG ATG GGC CAG AAT												435
Gly Thr Phe Asn Val Ile Arg Leu Val Ala Gly Glu Met Gly Gln Asn												
	125				130					135		
GAA CCA GAC CAG GGA GGC CAA CGT GGG GTC ATC ATC AAC ACT GCC AGT												483
Glu Pro Asp Gln Gly Gly Gln Arg Gly Val Ile Ile Asn Thr Ala Ser												
	140				145				150			155
GTG GCT GCC TTC GAG GGT CAG GTT GGA CAA GCT GCA TAC TCT GCT TCC												531
Val Ala Ala Phe Glu Gly Gln Val Gly Gln Ala Ala Tyr Ser Ala Ser												
	160							165			170	
AAG GGG GGA ATA GTG GGC ATG ACA CTG CCC ATT GCT CGG GAT CTG GCT												579
Lys Gly Gly Ile Val Gly Met Thr Leu Pro Ile Ala Arg Asp Leu Ala												
	175							180			185	
CCC ATA GGT ATC CGG GTG ATG ACC ATT GCC CCA GGT CTG TTT GGC ACC												627
Pro Ile Gly Ile Arg Val Met Thr Ile Ala Pro Gly Leu Phe Gly Thr												
	190							195			200	

CCA CTG CTG ACC AGC CTC CCA GAG AAA GTG TGC AAC TTC TTG GCC AGC	675
Pro Leu Leu Thr Ser Leu Pro Glu Lys Val Cys Asn Phe Leu Ala Ser	
205 210 215	
CAA GTG CCC TTC CCT AGC CGA CTG GGT GAC CCT GCT GAG TAT GCT CAC	723
Gln Val Pro Phe Pro Ser Arg Leu Gly Asp Pro Ala Glu Tyr Ala His	
220 225 230 235	
CTC GTA CAG GCC ATC ATC GAG AAC CCA TTC CTC AAT GGA GAG GTC ATC	771
Leu Val Gln Ala Ile Ile Glu Asn Pro Phe Leu Asn Gly Glu Val Ile	
240 245 250	
CGG CTG GAT GGG GCC ATT CGT ATG CAG CCT TGAAGGGAGA AGGCAGAGAA	821
Arg Leu Asp Gly Ala Ile Arg Met Gln Pro	
255 260	
AACACACGCT CCTCTGCCCT TCCTTTCCCT GGGGTACTAC TCTCCAGCTT GGGAGGAAGC	881
CCAGTAGCCA TTTTGTAACCT GCCTACCAGT CGCCCTCTGT GCCTAATAAA GTCTCTTTT	941
CTCACAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	981

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ala Ala Ala Cys Arg Ser Val Lys Gly Leu Val Ala Val Ile Thr
1 5 10 15

Gly Gly Ala Ser Gly Leu Gly Leu Ala Thr Ala Glu Arg Leu Val Gly
20 25 30

Gln Gly Ala Ser Ala Val Leu Leu Asp Leu Pro Asn Ser Gly Gly Glu
35 40 45

Ala Gln Ala Lys Lys Leu Gly Asn Asn Cys Val Phe Ala Pro Ala Asp
50 55 60

Val Thr Ser Glu Lys Asp Val Gln Thr Ala Leu Ala Leu Ala Lys Gly
65 70 75 80

Lys Phe Gly Arg Val Asp Val Ala Val Asn Cys Ala Gly Ile Ala Val
85 90 95

Ala Ser Lys Thr Tyr Asn Leu Lys Lys Gly Gln Thr His Thr Leu Glu
100 105 110

Asp Phe Gln Arg Val Leu Asp Val Asn Leu Met Gly Thr Phe Asn Val

115	120	125
Ile Arg Leu Val Ala Gly Glu Met Gly Gln Asn Glu Pro Asp Gln Gly 130 135 140		
Gly Gln Arg Gly Val Ile Ile Asn Thr Ala Ser Val Ala Ala Phe Glu 145 150 155 160		
Gly Gln Val Gly Gln Ala Ala Tyr Ser Ala Ser Lys Gly Gly Ile Val 165 170 175		
Gly Met Thr Leu Pro Ile Ala Arg Asp Leu Ala Pro Ile Gly Ile Arg 180 185 190		
Val Met Thr Ile Ala Pro Gly Leu Phe Gly Thr Pro Leu Leu Thr Ser 195 200 205		
Leu Pro Glu Lys Val Cys Asn Phe Leu Ala Ser Gln Val Pro Phe Pro 210 215 220		
Ser Arg Leu Gly Asp Pro Ala Glu Tyr Ala His Leu Val Gln Ala Ile 225 230 235 240		
Ile Glu Asn Pro Phe Leu Asn Gly Glu Val Ile Arg Leu Asp Gly Ala 245 250 255		
Ile Arg Met Gln Pro 260		

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 261 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Ala Ala Ala Cys Arg Ser Val Lys Gly Leu Val Ala Val Ile Thr 1 5 10 15
Gly Gly Ala Ser Gly Leu Gly Leu Ala Thr Ala Glu Arg Leu Val Gly 20 25 30
Gln Gly Ala Ser Ala Val Leu Leu Asp Leu Pro Asn Ser Gly Gly Glu 35 40 45
Ala Gln Ala Lys Lys Leu Gly Asn Asn Cys Val Phe Ala Pro Ala Asp 50 55 60

Val Thr Ser Glu Lys Asp Val Gln Thr Ala Leu Ala Leu Ala Lys Gly
65 70 75 80
Lys Phe Gly Arg Val Asp Val Ala Val Asn Cys Ala Gly Ile Ala Val
85 90 95
Ala Ser Lys Thr Tyr Asn Leu Lys Lys Gly Gln Thr His Thr Leu Glu
100 105 110
Asp Phe Gln Arg Val Leu Asp Val Asn Leu Met Gly Thr Phe Asn Val
115 120 125
Ile Arg Leu Val Ala Gly Glu Met Gly Gln Asn Glu Pro Asp Gln Gly
130 135 140
Gly Gln Arg Gly Val Ile Ile Asn Thr Ala Ser Val Ala Ala Phe Glu
145 150 155 160
Gly Gln Val Gly Gln Ala Ala Tyr Ser Ala Ser Lys Gly Gly Ile Val
165 170 175
Gly Met Thr Leu Pro Ile Ala Arg Asp Leu Ala Pro Ile Gly Ile Arg
180 185 190
Val Met Thr Ile Ala Pro Gly Leu Phe Gly Thr Pro Leu Leu Thr Ser
195 200 205
Leu Pro Glu Lys Val Cys Asn Phe Leu Ala Ser Gln Val Pro Phe Pro
210 215 220
Ser Arg Leu Gly Asp Pro Ala Glu Tyr Ala His Leu Val Gln Ala Ile
225 230 235 240
Ile Glu Asn Pro Phe Leu Asn Gly Glu Val Ile Arg Leu Asp Gly Ala
245 250 255
Ile Arg Met Gln Pro
260

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 255 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Asn Asp Leu Ser Gly Lys Thr Val Ile Ile Thr Gly Gly Ala Arg
1 5 10 15

Gly	Leu	Gly	Ala	Glu	Ala	Ala	Arg	Gln	Ala	Val	Ala	Ala	Gly	Ala	Arg
			20					25					30		
Val	Val	Leu	Ala	Asp	Val	Leu	Asp	Glu	Glu	Gly	Ala	Ala	Thr	Ala	Arg
		35					40				45				
Glu	Leu	Gly	Asp	Ala	Ala	Arg	Tyr	Gln	His	Leu	Asp	Val	Thr	Ile	Glu
	50					55					60				
Glu	Asp	Trp	Gln	Arg	Val	Val	Ala	Tyr	Ala	Arg	Glu	Glu	Phe	Gly	Ser
65					70					75				80	
Val	Asp	Gly	Leu	Val	Asn	Asn	Ala	Gly	Ile	Ser	Thr	Gly	Met	Phe	Leu
			85					90						95	
Glu	Thr	Glu	Ser	Val	Glu	Arg	Phe	Arg	Lys	Val	Val	Asp	Ile	Asn	Leu
			100					105					110		
Thr	Gly	Val	Phe	Ile	Gly	Met	Lys	Thr	Val	Ile	Pro	Ala	Met	Lys	Asp
		115				120						125			
Ala	Gly	Gly	Gly	Ser	Ile	Val	Asn	Ile	Ser	Ser	Ala	Ala	Gly	Leu	Met
	130					135					140				
Gly	Leu	Ala	Leu	Thr	Ser	Ser	Tyr	Gly	Ala	Ser	Lys	Trp	Gly	Val	Arg
145					150					155				160	
Gly	Leu	Ser	Lys	Leu	Ala	Ala	Val	Glu	Leu	Gly	Thr	Asp	Arg	Ile	Arg
			165					170						175	
Val	Asn	Ser	Val	His	Pro	Gly	Met	Thr	Tyr	Thr	Pro	Met	Thr	Ala	Glu
			180					185					190		
Thr	Gly	Ile	Arg	Gln	Gly	Glu	Gly	Asn	Tyr	Pro	Asn	Thr	Pro	Met	Gly
		195				200					205				
Arg	Val	Gly	Asn	Glu	Pro	Gly	Glu	Ile	Ala	Gly	Ala	Val	Val	Lys	Leu
	210					215					220				
Leu	Ser	Asp	Thr	Ser	Ser	Tyr	Val	Thr	Gly	Ala	Glu	Leu	Ala	Val	Asp
225					230					235				240	
Gly	Gly	Trp	Thr	Thr	Gly	Pro	Thr	Val	Lys	Tyr	Val	Met	Gly	Gln	
			245						250					255	

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Arg Gly Asp Ser

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